These constraints are based on the common structural elements in the binding or catalytic sites of these related proteins which form the site for conventional drug discovery. The common structural elements typically result in the selection of drugs that will inhibit the whole series of different proteins as these structural elements form the basis for the binding of the drug molecules selected from the screen. Thus conventional drug screening approaches result in the selection of drug hits which do not provide the degree of selectivity desired to bring about a desired therapeutic affect. In the subject invention, since the active site does not need to be the target for the selection of molecules that form the basis of the drug molecule, a significant improvement in the discovery of highly selective drugs is achieved. The consequence is the development of drugs with an enhanced therapeutic value. This advantage is further enhanced by the ability of this drug discovery approach to make use of the whole surface of the given protein target to find molecules with the desired binding specificity. This advantage is then combined with the ability to make use of a rapid screen that is wholly based on the use of binding and thus achieves a level of speed and through put not possible with other methods. This advantage is of great value when the desire is to find a very specific inhibitor of a given member of a protein family that is highly homologous and thus extremely difficult or impossible for drug discovery based on the effector, receptor or catalytic site of the given protein. This invention thus provides a means for the development of compounds of the invention which are

IN THE CLAIMS

Please cancel Claims 1-23, 31-35, 38, 39, 41 and 42 without prejudice.

Please substitute the following amended claims for corresponding claims previously presented. A copy of the amended claims showing current revisions is attached.